

**Table 1** Changes in microbiota composition associated with obesity.

Models	Disease	Implicated microbiota	Reference
Rat	Obesity	Altered gut microbiota	29,30
Rat	Obesity	<i>Firmicutes</i> ↑, <i>Bacteroidetes</i> ↓	31,32
Human	Obesity	<i>Firmicutes</i> ↑, <i>Bacteroidetes</i> ↓	37, 38, 39, 40, 41
Human	Obesity	<i>Proteobacteria</i> ↑, <i>Bacteroidetes</i> ↑, <i>Campylobacter</i> ↑, <i>Shigella</i> ↑, <i>Lactobacillus</i> ↑, <i>Clostridium coccoides</i> ↑, <i>Bifidobacterium</i> ↑, <i>Akkermansia muciniphila</i> ↓, <i>Clostridium leptum</i> ↓, <i>Bacteroides fragilis</i> ↓, <i>Bifidobacterium catenulatum</i> ↓	43,44
Human	Obesity	H <sub>2</sub> -producing <i>Prevotellaceae</i> ↑, H <sub>2</sub> -utilizing methanogenic <i>Archaea</i> ↑	46
Human	Obesity	<i>Enterobacter</i> ↑	48